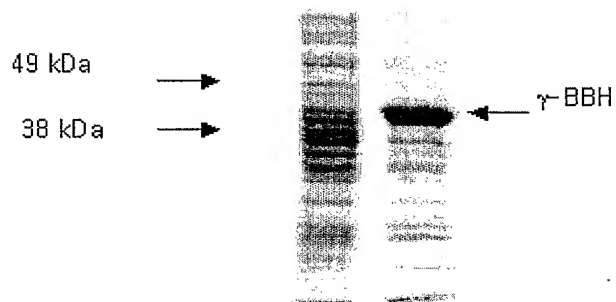


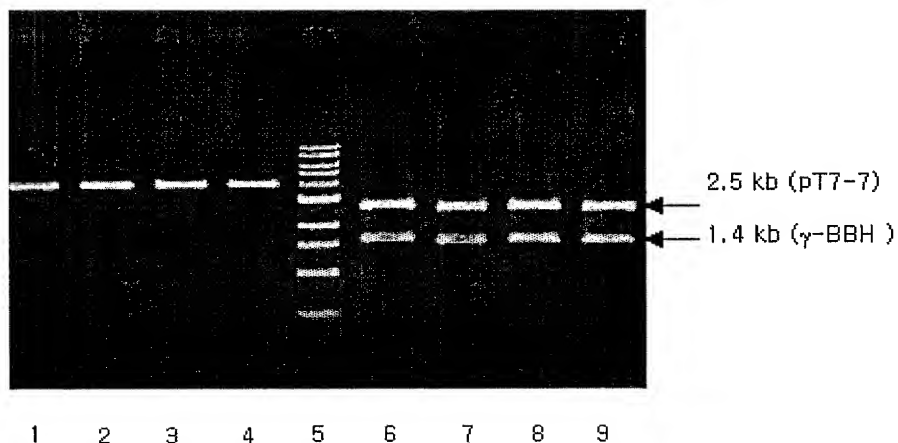
1/3

1



Lane 1 : Protein molecular size marker,  
 Lane 2 : E.coli BL21 w/o  $\gamma$ -BBH gene,  
 Lane 3 : E.coli BL21 w/  $\gamma$ -BBH gene and induced by 1mM IPTG

2



Lane 1~4 : pT7-7 + g-BBH plasmid digested with Nde I  
 Lane 5: 1kb DNA ladder  
 Lane 6~9 : pT7-7 + g-BBH plasmid digested with Nde I and Sal I

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3

CLUSTAL W (1.82) multiple sequence alignment

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Human      -----MACTIQKAEALDGAHLMQILWYDEEESLYPAVWLRDNCPCSDCYLDSAKARK 52
rat        -----MHCAILKAEAYDGAHLMQIFWHDGAESLYPAVWLRDNCQCSDCYLHSAKARK 52
pseudomonas NA IADVRTFPLI SPLASAA SFASGVSVTWADGRVSPFHNLWLRDNCPCGDCVVEVTREQV 60
N.crassa   -----MATAAVQVSVPAVVGQPDIGVAPDHDKYLARVKRRRENEKLESSLPFG---- 48
              :      . . .      ,      :      :      :      *      :      :

Human      LLVEALDYNIGIKGLIFDAK-KYVITWPDHYSEFQADWLKKRCFSKQARAKLQRELFFP 111
rat        LLEALDYNIRMDLTFDQK-KYVITWPNHVSFEFANWLKKRCFSQEARAGLQGEFLFP 111
pseudomonas FLVADVPEDIQVQAVTIGDDGRLVVQWDDGHASAYHPGWLRHAYDAQSLA---EREAAAP 118
N.crassa   -FPRRLDSDLVWDGNTLAETVDWTVRLTEEAIDEIEAALRHFKSLNKPLGVINQETFFLP 107
              :      :      :      :      :      :      :      :      :      :      *

Human      ECQYWGSELQLPTLDFEDVLRVDEHAYKWLSTLKKVGI VRLTGASDKPGEVSKLGKRMGF 171
rat        ECQYWGSELQLPTLNFEDVLRNDDHAYKWLSSLKKVGI VRLTGAADKRGELIKLGKRI GF 171
pseudomonas HKHRWMQGLSLPVYDHGAYMQDDDTLLEWLLAVRDVGLTQLHGVPTEPGALIPAKRISF 178
N.crassa   RLHHTLRSLSHLHHGHGFKYLR---GLPVTSTHTREENIIIVAGVSSHVAPIRGRQDNQ-H 164
              :      :      *      .      .      .      :      :      :      :      :      *      .      .      .

Human      LYLTFYGHWTQVQDKIDANNVAYTTGKLSFHTDYPALHHPGP-VQLLHCIKQTYTGGDSE 230
rat        LYLTFYGHWTQVQDKIDANNVAYTTGKLSFHTDYPALHHPGP-VQLLHCIKQTYTGGDSE 230
pseudomonas IRESNFGVLFQVRSKADADSNAYTAFNLPLHTDLPTRELQPG-LQFLHCLVNDATGGNST 237
N.crassa   NGHPADYVLAHIKDLSTTVSDYSKIGAPAYTTEKQVFHTDAGDIVALFCLGEAAEGGQSY 224
              :      :      :      :      :      :      *      :      :      :      *      :      :      :      :      :      :

Human      IVDGFNYCQKLKKNPQAFQILSS--TFVDFTDIGV-----DYCDFSVQSKHKIIELEDDK 283
rat        IVDGFNYCQKLKKNPQAFQILSS--TFVDFTDIGV-----DYCDFSVQSKHKIIELEDDK 283
pseudomonas FVDGFAIAEALRIEAPAAVRLCE--TPVEFRNK-----DRHSDVACTAPVIALDSS 287
N.crassa   LSSSWKVYNELAAATRPDLVRTLAEPWVADEFGEKGRKFSVRPLLHFQSTAAAAASREAKPE 284
              :      :      :      :      *      *      *      .      :      :      :      :      :      :      :

Human      GQVYRINFNNAIRDTIFDVP-VERVQPFYAALKEFVDLMN--SKESKFTFKMNPQGVITF 340
rat        GQVYRINFNNAIRDTVFDVP-IERVQPFYAALKEFVDLMN--SKEYKYTFKMNPQGVITF 340
pseudomonas GEVREIRLANFLR-APFQMD-AQRMPDYVYLAVRRFIQMTR--EPRFCFTRALEAGQLWCF 343
N.crassa   SERLI IQYARRFTGVWGLPRSADIPPI TEAQAEALDALHFTA EKYAYALDFRQGDVQFV 344
              :      :      *      .      :      :      :      :      *      :      :      :      :      :      :      :

Human      DNWRLLHGRRSYEAGTEISRHLEGAYAD-----WDVYMS-----RLRIL 379
rat        DNWRLLHGRRSYEAGTEISRHLEGAYAD-----WDVYMS-----RLRIL 379
pseudomonas DNRRLVLAHARDAFDP-ASGDRHFQGCYVD-----RDELLS-----RILVL 381
N.crassa   NNLVYFHSRAGFRDEGEKQRLVRLWLRDPENAWETPEALKERWERVYGGVSPEREVFP 404
              :      :      *      :      :      :      :      :      :      :      :      :      :      :      :      :

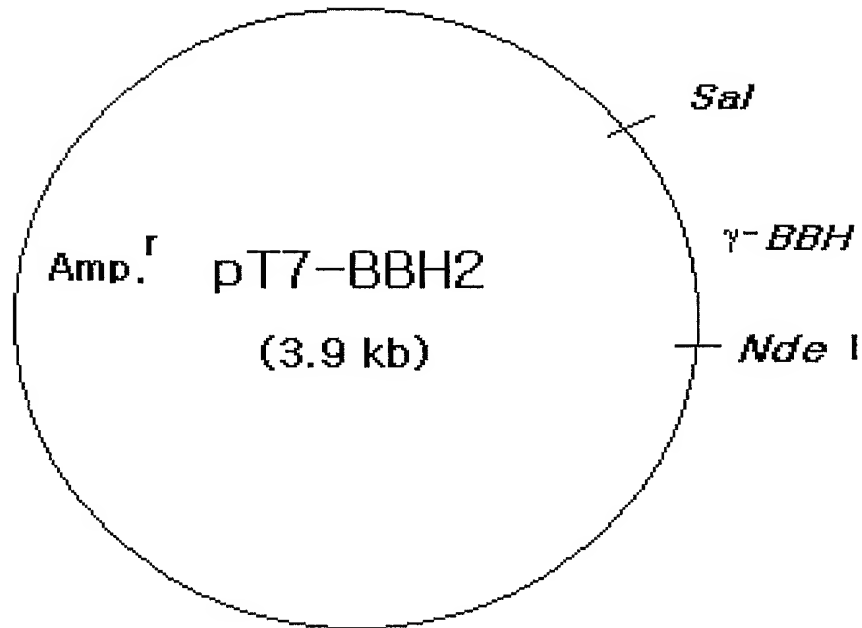
Human      RQRYENG----- 387
rat        RQRYMNG----- 387
pseudomonas QR----- 383
N.crassa   EPQIRASAKGESVGTQGGGGY 425

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(Sequences were aligned using the European Bioinformatics Institute (EMBL-EBI) sequence analysis program, clustalW.)

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4



5

